

SEQUENCE LISTING

<110> Lukyanov, Sergey

<120> FLUORESCENT PROTEINS FROM COPEPODA SPECIES AND METHODS FOR USING SAME

<130> COP_TEXT.DOC

<160> 30

<170> PatentIn version 3.1

<210> 1

<211> 1010

<212> DNA

<213> Pontellina plumata

<400> 1

```

agtctgctct ccaaaggata gacagtaaca ccaccaatat gcctgccatg aagattgagt      60
gccgcatacag tggaaacctg aacggagtggt tgtttgagct ggtcggaggt ggagaaggga      120
ttcctgagca gggacgtatg accaacaaga tgaagtctac caagggcgcc ttgaccttct      180
ccccctaect tctctctcat gtcattgggat acgggttcta ccactttggg acctatccca      240
gtgggtatga gaatcccttc ctgcatgccg ccaacaacgg ggggtacacc aacaccagga      300
ttgagaagta tgaggatgga ggagttcttc atgttagctt cagctacaga tatgaagcag      360
gcagggttat tggggatttc aaggttgtcg ggacaggatt ccttgaggac agtgtgatct      420
tcaccgacaa gatcatccgg tccaatgcta ccgtggagca cttgcaccca atgggagaca      480
acgttcttgt gggctccttc gcgagaacct ttcccttgag ggatggaggc tactactcat      540
ttgtggttga cagccacatg cacttcaaga gtgccatcca cccatccatc ctccagaacg      600
gggggtccat gtttgcttc aggagagttg aggaacttca ctccaacact gaacttggca      660
ttgtagagta tcaacatgcc tccaagaact ccacagcatt tgccatgaact agaaagtatc      720
aaatataaac agagtgacaa aggatctgtc gtcattctaa actttgtatg atttacaat      780
aatgatttaa tggcaactcc caaaatagac ttgaattaat tgaaaaatca actaaacata      840
atccttgttg ctctgttgat atgaacgctt tctgacttgg acccgggctt gaactgaccc      900
tgaaccacat cagacgaata acttgattct aaaattatat gaattttcaa acaaaacaat      960
ataatttggt aatgtgtaat catcttgaat aaacatatca gagaactcac      1010

```

<210> 2

<211> 222

<212> PRT

<213> Pontellina plumata

<400> 2

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Ser Gly Thr Leu Asn Gly
1           5           10           15
Val Val Phe Glu Leu Val Gly Gly Gly Glu Gly Ile Pro Glu Gln Gly
          20           25           30

```

Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
 50 55 60
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ala Asn Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
 130 135 140
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 3

<211> 1010

<212> DNA

<213> *Pontellina plumata*

<400> 3

agtctgctct ccaaaggata gacagtaaca ccaccaatat gcctgccatg aagattgagt 60
 gccgcatcac gggaaccctg aacggagtgg agtttgagct ggtcggaggt ggagaaggga 120
 ctcttgagca gggacgtatg accaacaaga tgaagtctac caagggcgcc ttgaccttct 180
 cccctacct tctctctcat gtcattggat acgggttcta ccacttttgt acctatccca 240
 gtgggtatga gaatcccttc ctgcatgcca tcaacaacgg ggggtacacc aacaccagga 300
 ttgagaagta tgaggatgga ggagttcttc atgttagctt tagctacaga tatgaagcag 360
 gcagggtgat tggggatttc aaggttgtcg ggacaggatt ccctgaggac agtgtgactt 420
 tcaccgacaa gatcatccgg tccaatgcta ccgtggagca cttagcaccct atgggagaca 480
 acgttcttgt gggctccttc gcgagaacct ttccctgag ggtatggaggc tactactcat 540
 ttgtggttga cagccacatg cacttcaaga gtgccatcca cccatccatc ctccagaacg 600

```

ggggggcccat gtttgcccttc aggagagttg aggaacttca ctccaacact gaacttggca      660
ttgtagagta tcaacatgcc tccaagactc ccatagcatt tgcctaaact acaaagtatc      720
aaatattaac agattgacaa aggatatgtc gtcattctaa actttgtatg atttacaat      780
aatgatttaa tgtcaaccct caaaataggc ttgaattaat tgaaaaaatca actaaacata      840
atccttggtg ctctgttgat atgaacactt tctgacttgg accccggcct gaactgaccc      900
tgaccacacat cagacgaaga acttgattct aagattatat gaattttcaa aaaaaacaat      960
atgatttggtt aatgtgtaat catcttgaat aaacatatca gagaacgcac      1010

```

<210> 4

<211> 222

<212> PRT

<213> Pontellina plumata

<400> 4

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65           70           75           80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85           90           95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115          120          125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
          130          135          140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145          150          155          160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
          165          170          175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
          180          185          190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
          195          200          205

```

Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala

210

215

220

<210> 5

<211> 814

<212> DNA

<213> Labidocera aestiva

<400> 5

```

cagtttcttc caagctaaat aaagaaacac atcaaaagca tcaacatgcc tgtcatgaag      60
attgagtgcc gtatctctgg aaccatgaac ggagaggagt ttgagcttgt aggagctggc      120
gatggaaaca ctgatgaagg acgtatgacc aacaagatga agtccaccaaa aggacctctc      180
tccctctctc cctacctact ctcccacatc atgggctacg gattctatca ctatgctacc      240
ttccctgctg gatatgagaa tgtctacctc catgctgcta agaattggagg ctacaccaac      300
accaggactg agaggtaaga agacggagga atcatttcgg tcaacttcac ctacagatat      360
gagggaaaca aggttatcgg agacttcaag gttgttggat caggattccc agctaacagt      420
gttatcttca ctgacaagat catcaagtcc aacccaacct gtgagcacat ctacccaag      480
ggagataata tctttgtcaa tgcctacact cgaacttggg tgcctgagaga tgggtggatac      540
tactctgcac aggtcaacaa tcctctccac ttcaagactg ccatgcaccc caccatgctc      600
cagaacggag gatccatgtt tacctacagg aaggttgagg agctccacag ccagtcagat      660
gttggtattg tagaatacca acatgtcttc aagaccccaa ctgcttttgc ctaagcttgg      720
aaatatgggt cctatcagac aattaatata ataaaattta cttatcattg taaaacccaaa      780
ctcttttaat gaataaattt ctgtatctac tact                                     814

```

<210> 6

<211> 222

<212> PRT

<213> Labidocera aestiva

<400> 6

```

Met Pro Val Met Lys Ile Glu Cys Arg Ile Ser Gly Thr Met Asn Gly
1           5           10           15
Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
35           40           45
Pro Tyr Leu Leu Ser His Ile Met Gly Tyr Gly Phe Tyr His Tyr Ala
50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Ala Lys Asn
65           70           75           80

```

Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
 85 90 95
 Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Ser Gly Phe Pro Ala Asn Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
 130 135 140
 Lys Gly Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Leu His Phe
 165 170 175
 Lys Thr Ala Met His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Lys Val Glu Glu Leu His Ser Gln Ser Asp Val Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 7
 <211> 753
 <212> DNA
 <213> cf. *Pontella meadi* Wheeler
 <400> 7

atcagttcat cagtacacga gcagagtcac acatcaaaat gccctgacatg aagcttgagt 60
 gccacatctc cggaaccatg aatggagagg agtttgaact tatctggctgct ggagatggaa 120
 atacagatga gggacgcatg accaacaaaa tgaagtcacat caaaggacct atctccttct 180
 ctccctacct cctctccac attcttggct acggatatta ccactttgca accctccctg 240
 ctggatatga aaatatctac cttcattcca tgaagaatgg aggttactcc aatgtcagaa 300
 ctgagaggta tgaggatgga ggcctcattt ctataacctt caactacaga tatgaaggga 360
 acaagatcat tggagacttc aaggttggtt gaacaggatt cctaccaaac agtccttatct 420
 tcactgacaa gatcattaaa tccaacctta cctgtgagaa catgttcccc aaggctgaca 480
 atactcttgt gaatgcctac accagaacat atttgcttaa agatgggtgga tactactctg 540
 cccagggtta caaccatctg cacttcaaga gtgccatcca taccaccatg ctccagaatg 600
 gcggatccat gttcacctac agagttgtag aggagacaca cactcagaac gaagttgcta 660
 ttgtagagta ccaaaatgtc tccaaaactc caactgcgtt tgcttgaaat acttgtaata 720
 aaactgcaaa gaaataaact aaattgtaca atc 753

<210> 8
 <211> 222

<212> PRT

<213> cf. Pontella meadi Wheeler

<400> 8

```

Met Pro Asp Met Lys Leu Glu Cys His Ile Ser Gly Thr Met Asn Gly
1           5           10           15
Glu Glu Phe Glu Leu Ile Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
20           25           30
Arg Met Thr Asn Lys Met Lys Ser Ile Lys Gly Pro Ile Ser Phe Ser
35           40           45
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
65           70           75           80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
85           90           95
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Asn Lys Ile Ile Gly
100          105          110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Thr Asn Ser Leu Ile Phe
115          120          125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
130          135          140
Lys Ala Asp Asn Thr Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
145          150          155          160
Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
165          170          175
Lys Ser Ala Ile His Thr Thr Met Leu Gln Asn Gly Gly Ser Met Phe
180          185          190
Thr Tyr Arg Val Val Glu Glu Thr His Thr Gln Asn Glu Val Ala Ile
195          200          205
Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala
210          215          220

```

<210> 9

<211> 880

<212> DNA

<213> cf. Pontella meadi Wheeler

<400> 9

```

tcctgtgttc cagtcattac cgggccctgt gaggaggaag agcacacaga caggagagta 60
taaatacaga gcggaagcac ggtgatcatc agttcctcag taaacgagta gagacacaca 120

```

```

tcaaaatgcc tgacatgaag cttgagtgcc acatctccgg aaccatgaat ggagaggagt 180
ttgaacttat tggttctgga gatggaaata ctgacaggg aagcatgaca aacaatatga 240
agtcacatcaa aggacctctc tccctctctc cctacctact cteccacatt cttggctatg 300
gatattacca ctttgcaacc ttcctgctg gatatgaaa tatoracct catgccatga 360
agaatggagg ttactcaaat gtcaggactg agaggatga ggatggaggc atcatttcta 420
taaccttcaa ctacagatat gaaggcagca agatcattgg agacttcaaa gttattggaa 480
caggattccc taccgacagt cttatcttca ctgacaagat cattaaatcc aacctacct 540
gcgagaacat gttccccaag gctgacaaca ttcttgtgaa tgcctacacc agaacctatt 600
tgcttaaaaga tgggtggatac tactctgccc aggttaacaa ccatatgcac ttcaagagtg 660
ccatccatcc tacaatgctc cagaatggtg gatccatggt cactcacaga gtagtagagg 720
agaaccacac taagaccaac gttgctatcg tagagtacca aaatgtcttc aaaactccta 780
ctgcatttgc ttaaaatact tgaacaaaa ctgcaagaa ataacctata ttgtacaata 840
gcattttatt aatgcataga aaaataaatg tatattttat 880

```

<210> 10

<211> 222

<212> PRT

<213> cf. *Pontella meadi* Wheeler

<400> 10

```

Met Pro Asp Met Lys Leu Glu Cys His Ile Ser Gly Thr Met Asn Gly
1           5           10           15
Glu Glu Phe Glu Leu Ile Gly Ser Gly Asp Gly Asn Thr Asp Gln Gly
20           25           30
Arg Met Thr Asn Asn Met Lys Ser Ile Lys Gly Pro Leu Ser Phe Ser
35           40           45
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
50           55           60
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
65           70           75           80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
85           90           95
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Ser Lys Ile Ile Gly
100          105          110
Asp Phe Lys Val Ile Gly Thr Gly Phe Pro Thr Asp Ser Leu Ile Phe
115          120          125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
130          135          140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
145          150          155          160

```

Lys	Asp	Gly	Gly	Tyr	Tyr	Ser	Ala	Gln	Val	Asn	Asn	His	Met	His	Phe
165								170				175			
Lys	Ser	Ala	Ile	His	Pro	Thr	Met	Leu	Gln	Asn	Gly	Gly	Ser	Met	Phe
180								185				190			
Thr	His	Arg	Val	Val	Glu	Glu	Asn	His	Thr	Lys	Thr	Asn	Val	Ala	Ile
195								200				205			
Val	Glu	Tyr	Gln	Asn	Val	Phe	Lys	Thr	Pro	Thr	Ala	Phe	Ala		
210								215				220			

```
<210> 11
<211> 847
<212> DNA
<213> Pontella mediterranea
<400> 11
```

agcagtggta	tcaacgcaga	gtacgcggga	gttctctaac	gaaaaccaag	agaaacagac	60
atcaagatgc	ccaacatgaa	gcttgagtgc	cgtatctccg	gaaccatgaa	tggagaggag	120
tttgaacttg	ttggtgctgg	agaaggaaac	actgatgagg	gacgcattgac	caacaagatg	180
aagtcaccca	agggacctct	ttcttctctt	ccttatttgc	tctcccacgt	tcttggttat	240
ggatactacc	actatgctac	cttccctgct	ggatatgaaa	atgtctacct	ccatgccatg	300
agaatggag	gttactccaa	cacaagaaat	gagaggatat	aggatggagg	tatcatctct	360
gctaccttca	actacagata	tgaagggaga	cagattcatg	gagacttcaa	ggttgtagga	420
acgggattcc	ctgccgacag	catcatcttc	actgacaaga	tcatcaagtc	caaccttacc	480
tgtgagcaca	tctaccccaa	ggctaacaat	attcttgtga	atgcttacac	cagaacctgg	540
atgcttagag	atggtggata	ctactctgcc	caggtcaaca	accacatgca	tttacagagt	600
gccattcatc	ccaccatgct	caagaatggg	ggatctatgt	tcacctacag	aaagggtgag	660
gagctccaca	cacaaactga	agtcgggtatt	gttgaatacc	agcatgtctt	caagaggcca	720
actgcttttg	cttaattttg	taaataaaga	aagaatctat	aatgcaatag	taccttaaag	780
ttttcaggat	aataaatata	taaagatttt	taataaaaaa	aaaaaaaaaa	aaaaaaaaaa	840
aaaaaaaa						847

```
<210> 12
<211> 222
<212> PRT
<213> Pontella mediterranea
<400> 12
```

Met	Pro	Asn	Met	Lys	Leu	Glu	Cys	Arg	Ile	Ser	Gly	Thr	Met	Asn	Gly
1				5					10					15	
Glu	Glu	Phe	Glu	Leu	Val	Gly	Ala	Gly	Glu	Gly	Asn	Thr	Asp	Glu	Gly
			20					25					30		

Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
 50 55 60
 Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
 65 70 75 80
 Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
 85 90 95
 Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
 130 135 140
 Lys Ala Asn Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Leu
 165 170 175
 Gln Ser Ala Ile His Pro Thr Met Leu Lys Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
 210 215 220

<210> 13

<211> 850

<212> DNA

<213> *Pontella mediterranea*

<400> 13

gcagtggtat caacgcagag tacgcgggga gttcctcaac gaaaaccgag agaaacatac 60
 atcaaaatgc cccacatgaa gcttgagtgc cgtatctccg gaaccatgaa cggagaggag 120
 ttgaaacttg ttggtgctgg agatggaaac actgatgagg gacgcatgac caaccagatg 180
 aagtcacaaa agggacctct ctcccttctct ccctaattgc tctccacgt tcttggtat 240
 ggatactacc actatgctac ctcccttgct ggatatgaaa atgtctacct ccattgcatg 300
 aagaatggag gttactcaa cacaagaact gagaggatg acgatggagg tatcatttct 360
 gctaccttca actacagata tgaagggaga cagattcatg gagacttcaa ggttggttga 420
 actggattcc ctgccgacag catcatcttc actgacaaga tcatcaagtc caaccctacc 480
 tgtgagcaca tctaccccaa ggctgacaat attcttgtga atgcctacac cagaacctgg 540
 atgcttagag atggtggata ctactctgct caggtaaca accacatgca cttaagagt 600

```

gccatccatc ccaccatgct ccagaatggt ggatctatgt tcacctacag aaagggttgag 660
gagctccaca cacaaactga agttggtatt gttgagtacc agcatgtttt caagaggccc 720
acagcttttg cttaattttg taaataaaga aagaatttat aatacaatag tgccttttatg 780
tttctaaaac aatgaatgta taaataaatc tcaaaatatt caaaaaaaaa aaaaaaaaaa 840
aaaaaaaaaa 850

```

```

<210> 14
<211> 222
<212> PRT
<213> Pontella mediterranea
<400> 14

```

```

Met Pro His Met Lys Leu Glu Cys Arg Ile Ser Gly Thr Met Asn Gly
1          5          10          15
Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
20          25          30
Arg Met Thr Asn Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
35          40          45
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
50          55          60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
65          70          75          80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile
85          90          95
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
100         105         110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
115         120         125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
130         135         140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145         150         155         160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
165         170         175
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
180         185         190
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
195         200         205
Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
210         215         220

```

<210> 15
 <211> 821
 <212> DNA
 <213> Unknown
 <220>
 <223> nucleic acid sequence for pdaelGFP from an unidentified
 Pontellidae species, complete cds
 <400> 15

```

atcagtttaa cttctttcag aagacaacta agacctacca acatggcagc catgaagatt      60
gagtgcagga tcaactggaac catgaacgga gtggagtttg agctggttgg aggaggagaa      120
ggaaatactg atcagggacg tatgaccaac aagatgaaat ctaccaaggg tccactctcc      180
tctctccct atcttctctc tcatgtcatg ggatatggat tctatcattt tggaacattt      240
cccagtgggt atgagaatcc ctatgtccac gccatgacga acggtggata taccaacacc      300
aggattgaaa gttatgaaga tggaggtgtt ctttacctta ccttcaacta cagattggat      360
ggaaacaaga ttatcgggga cttcaagtgt gtcggaactg gattccctga ggacagcgtt      420
atcttcaactg acaagatcat caagtccaac cccaattgtg aacatttcta tccaatggct      480
gaaaacatca tgaaaaatgc ctacatgaga actctctccc tcagagatgg tggctactac      540
tctggccagg ttaccagcca catccacttc aagaatgcga tccacccatc catccttcat      600
aacggcggat ccattgtcc cttacagaaga gttgaggagc tccacactca aactgatctt      660
ggaattgttg agtaccagca tgtattcaag actcccaactg cttttgcttg aatgccatga      720
agatgaaacc tgaacaagat caatctttat ttaccacaat atgtaaattg ttttaattgta      780
taattctcga gaattcatat aatacataga atttatctta c                                821

```

<210> 16
 <211> 222
 <212> PRT
 <213> Unknown
 <220>
 <223> amino acid sequence for pdaelGFP from an unidentified Pontellidae
 species
 <400> 16

```

Met Ala Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Met Asn Gly
1           5           10           15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Asn Thr Asp Gln Gly
          20           25           30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
          35           40           45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50           55           60

```

Thr Phe Pro Ser Gly Tyr Glu Asn Pro Tyr Val His Ala Met Thr Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Ser Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu Tyr Leu Thr Phe Asn Tyr Arg Leu Asp Gly Asn Lys Ile Ile Gly
 100 105 110
 Asp Phe Lys Cys Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Asn Cys Glu His Phe Tyr Pro
 130 135 140
 Met Ala Glu Asn Ile Met Lys Asn Ala Tyr Met Arg Thr Leu Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Gly Gln Val Thr Ser His Ile His Phe
 165 170 175
 Lys Asn Ala Ile His Pro Ser Ile Leu His Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Arg Val Glu Glu Leu His Thr Gln Thr Asp Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 17

<211> 669

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the humanized version of the ppluGFP2

<400> 17

atgcccgcga tgaagatcga gtgccgcac accggcaccc tgaacggcgt ggagttcgag 60
 ctggtgggag gggagagagg caccocccgag cagggccgca tgaccaacaa gatgaagagc 120
 accaagggcg ccccgacatt cagcccttac ctgctgagcc acgtgatggg ctacggcttc 180
 taccacttcg gcacctaccc cagcggctac gagaaccctt tcctgcacgc catcaacaac 240
 ggcggtctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300
 ttacgtctacc gctacgaggg cggccgcgtg atcggcgact tcaaggtggg gggcacccggc 360
 ttcccccagg acagcgtgat ctccaccgac aagatcatcc gcagcaacgc caccgtggag 420
 caccctgcacc ccattgggga taacgtgctg gtgggcagct tcgcccgcac ctccagcctg 480
 cgcgaaggcg gctactacag ctccgtgggt gacagccaca tgcaattcaa gagcgccatc 540
 caccocagca tcctgcagaa cgggggcccc atgttcgcct tccgccgcgt ggaggagctg 600
 cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca 660
 ttgcgctga 669

```
<210> 18
<211> 222
<212> PRT
<213> Artificial sequence
<220>
<223> amino acid sequence for the humanized version of the ppluGFP2
<400> 18
```

Met	Pro	Ala	Met	Lys	Ile	Glu	Cys	Arg	Ile	Thr	Gly	Thr	Leu	Asn	Gly
1				5					10					15	
Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	Glu	Gly	Thr	Pro	Glu	Gln	Gly
			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser
		35					40					45			
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly
	50					55					60				
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn
65					70					75				80	
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val
				85					90					95	
Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly
			100					105					110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe
	115						120					125			
Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	Thr	Val	Glu	His	Leu	His	Pro
	130				135						140				
Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser	Phe	Ala	Arg	Thr	Phe	Ser	Leu
145				150						155					160
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val	Val	Asp	Ser	His	Met	His	Phe
				165					170					175	
Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu	Gln	Asn	Gly	Gly	Pro	Met	Phe
		180					185						190		
Ala	Phe	Arg	Arg	Val	Glu	Glu	Leu	His	Ser	Asn	Thr	Glu	Leu	Gly	Ile
	195						200					205			
Val	Glu	Tyr	Gln	His	Ala	Phe	Lys	Thr	Pro	Ile	Ala	Phe	Ala		
	210				215						220				

<210>	19
<211>	589
<212>	DNA
<213>	Artificial sequence

<220>

<223> nucleic acid sequence for the ppluGFP2 with yeast-optimized codon usage

<400> 19

```

tactccagaa caaggtagaa tgactaataa aatgaaatct actaaagggtg ctttgacttt      60
ttctccatat ttgttggtctc atggtatggg ttatgggttt tatcattttg gtacttatcc      120
atctgggtat gaaaatccat ttttgcatgc tattaataat ggtgggttata ctaatactag      180
aattgaaaaa tatgaagatg gtggtgtttt gcattgttct ttttcttata gatattgaagc      240
tggttagagtt attggcgatt ttaaagtgtt tgggtactgg tttccagaag attctgttat      300
ttttactgat aaaattatta gatctaattg tactgttgaa catttgcac caatgggtga      360
taatgttttg gttgggttctt ttgctagaac tttttcttg agagatgggtg gttattattc      420
ttttgttggt gattctcata tgcattttaa atctgctatt catccatcta ttttgcaaaa      480
tggtgggtcca atgtttgctt ttagaagagt tgaagaattg cattctaata ctgaattggg      540
tattgttgaa tatcaacatg cttttaaaac tccaattgct tttgcttaa      589

```

<210> 20

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the ppluGFP2 with yeast-optimized codon usage

<400> 20

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1           5           10          15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
          20          25          30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
          35          40          45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
          50          55          60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65          70          75          80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
          85          90          95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
          100         105         110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
          115         120         125

```

Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
 130 135 140
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
 180 185 190
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
 210 215 220

<210> 21
 <211> 669
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> nucleic acid sequence for the CopCFP mutant
 <400> 21

atgcccgcca tgaagatcga gtgccgcata accggcaccc tgaacggcgt ggagttcgag 60
 ctggtgggag gaggagaggg cccccccgag caggggccgca tgaccaacaa gatgaagagc 120
 accaaaggcg cccctgacct cagccccctac ctgctgagcc acgtgatggg ctggggcttt 180
 taccacttcg gcacctaccc cagcggctac gagaacccct tcctgcacgc catcaacaac 240
 ggcggttaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300
 ttacgctacc gctacgagga cggccgcgtg atcggcgact tcaagggtgtt gggcaccggc 360
 ttccccgagg acagcgtgat ctccaccgac aagatcatcc gcagcaacgc caccgtggag 420
 cacctgcgcc ccatgggcga taacgtgctg gtgggcagct tcgccgcac ctccagcctg 480
 cgcgacggcg gtactacag ctccgtggtg gacagccaca tgcacttcaa gagcgccatc 540
 cccccagca tcctgcagaa cgggggcccc atgttcgect tcgccgcgt ggaggagctg 600
 cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgaccgca 660
 ttgccttaa 669

<210> 22
 <211> 222
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> amino acid sequence for the CopCFP mutant
 <400> 22

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
 1 5 10 15
 Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
 20 25 30
 Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly
 50 55 60
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro
 130 135 140
 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
 180 185 190
 Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
 195 200 205
 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 23

<211> 690

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NAl variant

<400> 23

atggagagcgc acgagagcgg cctgcccgcgc atggagatcg agtgccgcac caccggcacc 60
 ctgaacggcgc tggagtgcga gctggtgggc gccggagagg gcacccccga gcaggggccgc 120
 atgaccaaca agatgaagag caccaagggc gccctgacct tcagccocta cctgctgagc 180
 cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc 240


```

ttcctgcacg ccatacaaaa cggcgggtac accaacaccc gcacgcagaa gtaacaggac 300
ggcggcgtgc tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac 360
ttcaaggtgg tgggcacccg cttccccgag gacagcgtga tcttcaccga caagatcctc 420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc 480
ttcgcccgca ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac 540
atgcacttca agagcgccat ccaccccagc atcctgcaga acggggggccc catgttcgcc 600
ttccgcccgc tggaggagct gcacagcaac accgagctgg gcacgtgga gtaccagcac 660
gccttcaaga ccccgatcgc attcgctga 690

```

<210> 24

<211> 229

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NAL variant

<400> 24

```

Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1           5           10           15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
          20           25           30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
          35           40           45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
          50           55           60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65           70           75           80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
          85           90           95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
          100          105          110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
          115          120          125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
          130          135          140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145          150          155          160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
          165          170          175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
          180          185          190

```

Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
 195 200 205
 Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
 210 215 220

Pro Ile Ala Phe Ala

225

<210> 25

<211> 819

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA2 variant

<400> 25

```

atgcccgcga tgaagatcga gtgccgcac accggcacc tgaacggcgt ggagttcgag      60
ctggctggggcg gcggagaggg ccccccgag cagggccgca tgaccaacaa gatgaagagc      120
accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc      180
taccacttcg gcacctacc cagcggctac gagaaccctt tcctgcacgc catcaacaac      240
ggcggtctaca ccaacacccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc      300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc      360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag      420
cacctgcacc ccattgggca taacgtgctg gtgggcagct tcgcccgcac cttcagcctg      480
cgcgacggcg gctactacag cttcgtgggt gacagccaca tgcacttcaa gagcgccatc      540
caccaccagca tcctgcagaa cgggggcccc atgttcgcct tcgcgcgcgt ggaggagctg      600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac ccgatcgca      660
ttcgccagat ccagagccca ggccagcaac tcgcgcgtgg atggcacagc cggaccggga      720
tcggccgcga cctagatca taatcagcca taccacattt gtagagggtt tacttgcttt      780
aaaaaacctc ccacacctcc ccctgaacct gaaacataa      819

```

<210> 26

<211> 272

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA2 variant

<400> 26

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
 1 5 10 15

Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	Glu	Gly	Thr	Pro	Glu	Gln	Gly
			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Ala	Leu	Thr	Phe	Ser
		35					40					45			
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly
	50					55					60				
Thr	Tyr	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Phe	Leu	His	Ala	Ile	Asn	Asn
65					70					75				80	
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Lys	Tyr	Glu	Asp	Gly	Gly	Val
			85						90					95	
Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	Glu	Ala	Gly	Arg	Val	Ile	Gly
		100						105					110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe
	115						120					125			
Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	Thr	Val	Glu	His	Leu	His	Pro
	130					135						140			
Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser	Phe	Ala	Arg	Thr	Phe	Ser	Leu
145				150						155					160
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Phe	Val	Val	Asp	Ser	His	Met	His	Phe
			165						170					175	
Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu	Gln	Asn	Gly	Gly	Pro	Met	Phe
		180						185					190		
Ala	Phe	Arg	Arg	Val	Glu	Glu	Leu	His	Ser	Asn	Thr	Glu	Leu	Gly	Ile
	195						200						205		
Val	Glu	Tyr	Gln	His	Ala	Phe	Lys	Thr	Pro	Ile	Ala	Phe	Ala	Arg	Ser
	210						215					220			
Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ala	Val	Asp	Gly	Thr	Ala	Gly	Pro	Gly
225				230						235					240
Ser	Ala	Ala	Thr	Leu	Asp	His	Asn	Gln	Pro	Tyr	His	Ile	Cys	Arg	Gly
			245						250					255	
Phe	Thr	Cys	Phe	Lys	Lys	Pro	Pro	Thr	Pro	Pro	Pro	Glu	Pro	Glu	Thr
		260						265					270		

<210> 27

<211> 840

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence for the CopGFP-NA3 variant

<400> 27

atggagagcgc acgagagcgcg cctgcccgcgc atggagatcgc agtgcgcgcac caccgcgcacc

60

```

ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc 120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc 180
cacgtgatgg gctacgggtt ctaccacttc ggcaacctacc ccagcggcta cgagaacccc 240
ttcctgcacg ccatcaacaa cggcgggtac accaacaccc gcacgcagaa gtacgaggac 300
ggcggcgtgc tgcacgtgag cttcagctac cgtacgagg ccggccgcgt gatcggcgac 360
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcacc 420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc 480
ttcgccccga ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac 540
atgcacttca agagcgccat ccaccccagc atcctgcaga acggggggccc catgttcgcc 600
ttccgcccgc tggaggagct gcacagcaac accgagctgg gcacgtgga gtaccagcac 660
gccttcaaga ccccgatcgc attogccaga tccagagccc aggccagcaa ctccgcctg 720
gatggcacag ccggaccggg atcggccgcg actctagatc ataatcagcc ataccacatt 780
tgtagaggtt ttacttgctt taaaaaacct cccacacctc cccctgaacc tgaacataa 840

```

<210> 28

<211> 279

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence for the CopGFP-NA3 variant

<400> 28

```

Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1           5           10           15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
20           25           30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
35           40           45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
50           55           60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65           70           75           80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
85           90           95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
100          105          110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
115          120          125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
130          135          140

```

Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
 145 150 155 160
 Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
 165 170 175
 Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
 180 185 190
 Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
 195 200 205
 Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
 210 215 220
 Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val
 225 230 235 240
 Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln
 245 250 255
 Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr
 260 265 270
 Pro Pro Pro Glu Pro Glu Thr
 275

<210> 29

<211> 238

<212> PRT

<213> Aequorea victoria

<400> 29

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130	135	140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145	150	155
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		
165	170	175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
180	185	190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
195	200	205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
210	215	220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys		
225	230	235

<210> 30
 <211> 225
 <212> PRT
 <213> Discosoma sp.

<400> 30

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val		
1	5	10
Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu		
20	25	30
Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val		
35	40	45
Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln		
50	55	60
Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro		
65	70	75
Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val		
85	90	95
Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser		
100	105	110
Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn		
115	120	125
Phe Pro Ser Asp Gly Pro Val-Met Gln Lys Lys Thr Met Gly Trp Glu		
130	135	140

[illegible]